

Run on: March 14, 2003, 05:19:53 ; Search time 1.04494 Seconds
 (without alignments)
 827.996 Million cell updates/sec

OM protein - protein search, using sw model

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GenCore version 5.1.3

title: US-09-698-781-17
perfect score: 44
sequence: 1 TLFPVLLFL 9
Scoring table: BLOSUM62
Gapop: 10.0 , Gapext: 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

PIR_73:*
 1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	44	100.0	245	S68691
2	36	81.8	161	neutrophil granules matrix glycoprotein SGP28 precursor - human
3	36	81.8	408	neutrophil granules matrix glycoprotein SGP28 precursor - human
4	35	79.5	222	neutrophil granules matrix glycoprotein SGP28 precursor - human
5	35	79.5	227	neutrophil granules matrix glycoprotein SGP28 precursor - human
6	35	79.5	361	neutrophil granules matrix glycoprotein SGP28 precursor - human
7	35	79.5	1325	neutrophil granules matrix glycoprotein SGP28 precursor - human
8	35	79.5	174	neutrophil granules matrix glycoprotein SGP28 precursor - human
9	34	77.3	2	neutrophil granules matrix glycoprotein SGP28 precursor - human
10	34	77.3	227	neutrophil granules matrix glycoprotein SGP28 precursor - human
11	34	77.3	237	neutrophil granules matrix glycoprotein SGP28 precursor - human
12	34	77.3	247	neutrophil granules matrix glycoprotein SGP28 precursor - human
13	34	77.3	301	neutrophil granules matrix glycoprotein SGP28 precursor - human
14	34	77.3	330	neutrophil granules matrix glycoprotein SGP28 precursor - human
15	34	77.3	405	neutrophil granules matrix glycoprotein SGP28 precursor - human
16	34	77.3	405	neutrophil granules matrix glycoprotein SGP28 precursor - human
17	34	77.3	511	neutrophil granules matrix glycoprotein SGP28 precursor - human
18	34	77.3	653	neutrophil granules matrix glycoprotein SGP28 precursor - human
19	34	77.3	741	neutrophil granules matrix glycoprotein SGP28 precursor - human
20	33	75.0	89	neutrophil granules matrix glycoprotein SGP28 precursor - human
21	33	75.0	303	neutrophil granules matrix glycoprotein SGP28 precursor - human
22	33	75.0	305	neutrophil granules matrix glycoprotein SGP28 precursor - human
23	33	75.0	365	neutrophil granules matrix glycoprotein SGP28 precursor - human
24	33	75.0	365	neutrophil granules matrix glycoprotein SGP28 precursor - human
25	33	75.0	459	neutrophil granules matrix glycoprotein SGP28 precursor - human
26	33	75.0	483	neutrophil granules matrix glycoprotein SGP28 precursor - human
27	33	75.0	668	neutrophil granules matrix glycoprotein SGP28 precursor - human
28	33	75.0	744	neutrophil granules matrix glycoprotein SGP28 precursor - human
29	33	75.0	1007	neutrophil granules matrix glycoprotein SGP28 precursor - human

ALIGNMENTS

RESULT 1	Query	Match	Length	DB ID	Description
S68691	1 TLFPVLLFL 9	100.0%	245	S68691	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	161	E82044	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	408	T39570	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	222	F90624	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	361	D72389	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	1325	T01037	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	174	A70407	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	227	T1185	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	237	H84035	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	247	JE0307	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	301	S12064	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	330	T34250	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	405	G97072	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	405	B89976	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	511	AG1912	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	653	G82971	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	741	T1303	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	89	B88683	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	161	A43708	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	408	D84912	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	227	D71559	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	365	B81713	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	365	E82044	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	459	A9932	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	483	G71523	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	668	E96777	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	744	T12705	neutrophil granules matrix glycoprotein SGP28 precursor - human
S68691	1 TLFPVLLFL 9	100.0%	1007	PN0156	neutrophil granules matrix glycoprotein SGP28 precursor - human

RESULT 2

Query	Match	Length	DB ID	Description	
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	245	S68691	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	161	E82044	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	408	T39570	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	222	F90624	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	361	D72389	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	1325	T01037	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	174	A70407	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	227	T1185	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	237	H84035	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	247	JE0307	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	301	S12064	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	330	T34250	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	405	G97072	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	405	B89976	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	511	AG1912	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	653	G82971	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	741	T1303	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	89	B88683	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	161	A43708	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	408	D84912	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	227	D71559	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	365	B81713	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	365	E82044	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	459	A9932	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	483	G71523	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	668	E96777	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	744	T12705	neutrophil granules matrix glycoprotein SGP28 precursor - human
1 TLFPVLLFL 9	1 TLFPVLLFL 9	100.0%	1007	PN0156	neutrophil granules matrix glycoprotein SGP28 precursor - human

A; Reference number: A82035; MUID:20406833; PMID:10952301
 A; Accession: E82044
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-161 <HIT>
 A; Cross-references: GB:AE004335; GB:AE003852; NID:99657289; PIDN:AAF95837.1; GSPPDB:GN001
 C; Genetics:
 A; Gene: VC696
 A; Map position: 1
 C; Superfamily: Escherichia coli hypothetical protein b4140
 Query Match^h
 Best Local Similarity 81.8%; Score 36; DB 2; Length 161;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFPVVLFL 9
 Db 1 MFPILLFL 8

RESULT 3
 T39570 probable metal transporter - fission yeast (schizosaccharomyces pombe)
 C; Species: Schizosaccharomyces pombe
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
 C; Accession: T39570
 R; Wood, V.; Rolandream, M.A.; Barrell, B.G.; Brown, D.; Churcher, C.M.
 Submitted to the EMBL Data Library, March 1999
 A; Reference number: 221864
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-408 <HOT>
 A; Cross-references: EMBL:AL035637; PIDN: CAB39510.1; GSPPDB:GN00067; SPDB:SPBC16D10.05
 C; Genetics:
 A; Gene: SDBB:SPBC16D10.05
 A; Map position: 2

Query Match^h
 Best Local Similarity 75.0%; Score 36; DB 2; Length 408;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLFPVLF 8
 Db 281 TLFPVLF 288

RESULT 4
 G72297 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C; Species: Thermotoga maritima
 C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C; Accession: G72297
 R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, C.M.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 Nature 399, 323-329, 1999
 A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A; Reference number: A72200; MUID:99287316; PMID:10360571
 A; Accession: D72384
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-361 <HOT>
 A; Cross-references: GB:AE001718; GB:AE000512; NID:94980881; PIDN:AAD35473.1; PID:9491
 C; Genetics:
 A; Gene: TM0388

Query Match^h
 Best Local Similarity 75.0%; Score 35; DB 2; Length 361;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFPVVLFL 9
 Db 25 LFPILLFL 32

RESULT 5
 F90624 ATP synthase F0 chain 6 [imported] - Casuarius casuarius mitochondrion
 C; Species: mitochondrion Casuarius casuarius
 C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 03-Aug-2001
 C; Accession: F90624
 R; Hadzirath, O.; Baker, A.J.
 Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001
 A; Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogeny
 A; Reference number: A99613; MUID:21263106; PMID:11370967
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-127 <HOT>
 A; Cross-references: GB:NC_002778; NID:914141864; PIDN:NP_115355.1; GSPPDB:GN00162
 C; Genetics:
 A; Gene: ATP6
 A; Genome: mitochondrion
 A; Genetic code: SGC1
 C; Superfamily: H+-transporting ATP synthase protein 6
 C; Keywords: mitochondrion
 Query Match^h
 Best Local Similarity 100.0%; Score 35; DB 2; Length 227;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFPVVLFL 8
 Db 25 LFPVLF 31

RESULT 6
 D72384 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C; Species: Thermotoga maritima
 C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C; Accession: D72384
 R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, C.M.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 Nature 399, 323-329, 1999
 A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A; Reference number: A72200; MUID:99287316; PMID:10360571
 A; Accession: D72384
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-361 <HOT>
 A; Cross-references: GB:AE001718; GB:AE000512; NID:94980881; PIDN:AAD35473.1; PID:9491
 C; Genetics:
 A; Gene: TM0388

Query Match^h
 Best Local Similarity 75.0%; Score 35; DB 2; Length 361;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LFPVVLFL 9
 Db 25 LFPILLFL 32

RESULT 7
 E89839 hypothetical protein SA0639 [imported] - staphylococcus aureus (strain N315)
 C; Species: Staphylococcus aureus
 C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C; Accession: E89839

Query Match^h
 Best Local Similarity 75.0%; Score 35; DB 2; Length 222;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 A; Gene: TM1087

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet, 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant staphylococcus aureus.
A;Reference number: A89758; MVID:2131952; PMID:11418146
A;Accession: EG9839
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-543 <UNK>
A;Cross-references: GB:BA000018; PID:913700575; PIDN:BAB41872.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0639

RESULT 8
T0137
hypothetical protein YUP8H12R_20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999
C;Accession: T0137
C;Title: Multiple independent origins of mitochondrial gene order in birds.
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrial; Oefner, P.; Davis, R.W.
C;Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
C;Status: translated from GB/EMBL/DBDJ
A;Residues: 1-1325 <THE>
A;Cross-references: EMBL:AC002986; NID:92494106; PID:93152582; GSPDB:GN00059; ATSP:YUP8H12R_20
A;Genetics:
A;Gene: ATSP:YUP8H12R_20
A;Map position: 1
A;Introns: 70/2; 130/3; 233/3; 384/3; 450/3; 470/1; 687/3; 740/3; 765/3; 868/3; 940/3; 1
Query Match 79.5%; Score 35; DB 2; Length 1325;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 TLFPVVLF 9
Db 72 TLFPLLL 80

RESULT 9
A70447
conserved hypothetical protein aq_1706 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
C;Accession: A70447
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V;Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MVID:98196666; PMID:9537320
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-174 <AOF>
A;Cross-references: GB:AE000052; NID:92984021; PIDN:AC07576.1; PID:92984033; GB:AE00065
C;Genetics:
A;Gene: aq_1706

RESULT 10
T1185
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - Smithornis sharpei mitoc
C;Species: mitochondrion Smithornis sharpei
C;Accession: T1185
R;Mindell, D.P.; Sorenson, M.D.; Blench, D.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 10693-10697, 1998
A;Title: Multiple independent origins of mitochondrial gene order in birds.
A;Reference number: Z17242
A;Accession: T1185
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Cross-references: EMBL:AF090340; NID:94894488; PID:94894494; PIDN:AA032519.1
A;Genetics:
A;Gene: mitochondrial
A;Map position: 1-227 <MIN>
A;Introns: 1
Query Match 77.3%; Score 34; DB 2; Length 227;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TLFPVVLF 8
Db 24 TLFPMLY 31

RESULT 11
H84035
hypothetical protein BH3088 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Accession: H84035
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MVID:20512582; PMID:11058132
A;Accession: H84035
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <STO>
A;Cross-references: GB:AP001517; GB:BA000004; NID:91017550; PIDN:BA06807.1; GSPDB:
C;Genetics:
C;Gene: BH3088
C;Superfamily: Bacillus subtilis hypothetical protein yoaT
Query Match 77.3%; Score 34; DB 2; Length 237;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy 2 LFPVVLFL 9
Db 16 LFPVVIFL 23

RESULT 12
JB0307
membrane protein - rat

C; Species: *Rattus norvegicus* (Norway rat)
 C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
 C; Accession: JE0307
 R; Nakada, T.; Kishimoto, T.; Kokura, K.; Okawa, N.; Makino, Y.; Muramatsu, M.; Tamura, DNA Res. 5, 315-317, 1998
 A; Title: Cloning of a novel rat gene, DB83, that encodes a putative membrane protein.
 A; Reference number: JE0307; MUID:99087491; PMID:9872456
 A; Accession: JE0307
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-247 <HAR>
 A; Cross-references: DDBJ:AB006135

Query Match 77.3%; Score 34; DB 2; Length 247;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TLFPVILF 8
 Db 111 SIFPVLLF 118

RESULT 13

SL2864
 retinal isomerase (EC 5.2.1.3) [validated] - Japanese flying squid
 N; Alternate names: retinohchrome
 C; Species: *Todirodes pacificus* (Japanese flying squid)
 C; Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 01-Sep-2000
 C; Accession: SL2864; S36449
 R; Hara-Nishimura, I.; Matsumoto, T.; Mori, H.; Nishimura, M.; Hara, R.; Hara, T.
 FEBs Lett. 271, 106-110, 1990
 A; Title: Cloning and nucleotide sequence of cDNA for retinohrome, retinal photoisomers
 A; Reference number: SL2864; MUID:91032043; PMID:2226795
 A; Accession: SL2864
 A; Molecule type: mRNA
 A; Residues: 1-301 <HAR>
 A; Cross-references: EMBL:X57143; NID:910776; PID:910777
 R; Hara-Nishimura, I.; Kondo, M.; Nishimura, M.; Hara, R.; Hara, T.
 FEBs Lett. 315, 94-98, 1993
 A; Title: Amino acid sequence surrounding the retinal-binding site in retinohrome of the A; Reference number: S39449; MUID:94063090; PMID:8243675
 A; Accession: S39449
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 274-277, 'X', 279-282 <HAR>
 C; Superfamily: vertebrate rhodopsin
 C; Keywords: chromoprotein; cis-trans-isomerase; G protein-coupled receptor; glycoprotein
 C; 1-301/Product: retinal isomerase #status experimental <MAT>
 F; 19-43/domain: transmembrane #status predicted <TM1>
 F; 54-75/domain: transmembrane #status predicted <TM2>
 F; 95-120/domain: transmembrane #status predicted <TM3>
 F; 133-153/domain: transmembrane #status predicted <TM4>
 F; 181-208/domain: transmembrane #status predicted <TM5>
 F; 231-255/domain: transmembrane #status predicted <TM6>
 F; 265-288/domain: transmembrane #status predicted <TM7>
 F; 170/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 275/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 77.3%; Score 34; DB 1; Length 301;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 LFPVILFL 9
 Db 280 LFPVILFL 287

RESULT 14

T34250
 hypothetical protein F31D5.6 - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C; Accession: T34250

R; Wilcox, L. submitted to the EMBL Data Library, June 1995
 A; Description: The sequence of *C. elegans* cosmid F31D5.
 A; Reference number: Z21194
 A; Accession: T34250
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-330 <HIL>
 A; Cross-references: EMBL:U28941; PIDN:AC71104.1; GSDB:GN00020; CESP:F31D5.6
 A; Experimental source: strain Bristol N2; clone F31D5
 A; Genetics:
 A; Gene: CESP:F31D5.6
 A; Map Position: 2
 A; Introns: 28/2; 45/1; 79/2; 158/1; 223/3; 281/2
 A; Introns: 28/2; 45/1; 79/2; 158/1; 223/3; 281/2
 Query Match 77.3%; Score 34; DB 2; Length 330;
 Best Local Similarity 77.8%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 TLFPVILFL 9
 Db 211 TFPVILFL 219

RESULT 15

G97072
 uncharacterized conserved protein CAC1402 (similar to Icac of *Staphylococcus* and YHUR
 C; Species: *Clostridium acetobutylicum* C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001
 C; Accession: G97072
 R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Makarova, K.S.; Zeng, Q.; Gibson, R.; I
 J. Bacteriol. 183, 4823-4838, 2001
 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
 A; Reference number: A96500; MUID:2135925; PMID:21359325
 A; Accession: G97072
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-356 <KUR>
 A; Cross-references: GB:AE001437; PIDN:AAK79370.1; PID:915024340; GSDB:GN00168
 A; Experimental source: *Clostridium acetobutylicum* ATCC824
 A; Genetics:
 A; Gene: CAC1402

Query Match 77.3%; Score 34; DB 2; Length 356;
 Best Local Similarity 85.7%; Pred. No. 54;
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 Qy 2 LFPVILFL 8
 Db 23 LFPVILFL 29

Search completed: March 14, 2003, 05:41:35
 Job time : 4.04494 secs